

SEQUENCE LISTING

<110> Hallahan, David L.

<120> cis-Prenyltransferases from Plants

<130> BC1019 US NA

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<150> 60/155,046

<151> 1999-09-21

<160> 37

<170> Microsoft Office 97

<210> 1

<211> 1388

<212> DNA

<213> Dimorphotheca

<400> 1

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<211> 287

<212> PRT

<213> Dimorphotheca

<400> 2

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20 25 30

Ser Asp Thr Thr Gly Gly Ile Asn Ser Leu Glu Glu Arg Ile Thr
35 40 45

Pro	Ala	Gly	Leu	Lys	His	Glu	Leu	Met	Pro	Lys	His	Val	Ala	Val	Ile
50						55				60					
Met	Asp	Gly	Asn	Arg	Arg	Trp	Ala	Arg	Ser	Arg	Gly	Leu	Met	Pro	Asp
65						70				75				80	
Ala	Gly	Tyr	Met	Glu	Gly	Ala	Arg	Ser	Leu	Lys	Val	Met	Val	Glu	Leu
						85				90				95	
Cys	Arg	Lys	Trp	Gly	Ile	Gln	Val	Leu	Thr	Val	Phe	Ala	Phe	Ser	Ala
						100				105				110	
Asp	Asn	Trp	Leu	Arg	Pro	Lys	Val	Glu	Val	Asp	Phe	Leu	Met	Gly	Leu
						115				120				125	
Ile	Glu	Ser	Val	Leu	Lys	Asp	Glu	Val	Val	His	Met	Ile	Lys	Glu	Gly
						130				135				140	
Ile	Gln	Leu	Ser	Val	Ile	Gly	Asp	Thr	Ser	Lys	Leu	Pro	Lys	Ser	Val
						145				150				155	
Lys	Arg	Ile	Ile	Thr	Tyr	Ala	Glu	Asn	Ile	Thr	Lys	Asn	Asn	Ser	Gln
						165				170				175	
Leu	Asn	Leu	Val	Val	Ala	Ile	Asn	Tyr	Ser	Gly	Lys	Tyr	Asp	Ile	Val
						180				185				190	
Gln	Ala	Cys	Gln	Ser	Ile	Ala	Leu	Lys	Val	Lys	Asp	Gly	Val	Ile	Gln
						195				200				205	
Pro	Glu	Glu	Ile	Asn	Glu	Phe	Thr	Ile	Glu	Asn	Glu	Leu	Gly	Thr	Asn
						210				215				220	
Cys	Ile	Pro	Phe	Pro	His	Pro	Asp	Leu	Leu	Ile	Arg	Thr	Ser	Gly	Glu
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Leu	Arg	Val	Ser	Asn	Phe	Phe	Leu	Trp	Gln	Leu	Ala	Tyr	Thr	Glu	Leu
						245				250				255	
Tyr	Phe	Ser	Glu	Thr	Leu	Trp	Pro	Asp	Phe	Gly	Glu	Asp	Glu	Leu	Leu
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 <212> DNA
 <213> Calendula officinalis

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 ttacaaat atcaacgggtt ttgagcaatg aaaataccaa actgaaaacc aaaaaaaagaa 180
 gaagtagaaat taccagggggg tctcgaagaa gaactaatgc caaaacacgt tgcattcata 240
 atggatggaa accgtcgatg ggcgggtggaa aaagggttgggt ctccaatgac gggtcatagt 300
 gccatgagaa agacgcttca atctctcctt ttgcgtatgtt ccaaattcaa aatcaaagcg 360
 gtatcgattt atgcattttc taccgaaaat tggactcgcc cgaaggaaga agttgatttc 420
 ctaatggaga tttatggagg acagatgctg aggagcttta aagtcttgggt 480
 tttcgatggaa gcataatggg gaaaaagacc aaccttccga aatcactaca aaagttatgc 540
 atcgaaatag aaaaaaaatc aagagccat tcaggaacccc atgttaacta tgcactcaac 600
 tacagtggaa aatacgacat aatcgaagct tttaaaagcg tcgctacaaa agtcaaggat 660

ggtgttatta	ttccaaaaca	gatcgacgaa	aaatatttca	aacaagaact	cggtacccaa	720
atgatcgatt	ttccttaccc	tgacctagtt	atacgtacaa	gcggggaaat	taggcttagt	780
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gattttgggg	aaaatgatct	tatcgaggct	ttacttgcatt	ttcaaaaagt	gcgtaaatgt	900
taataacttg	ttgtggttaa	gacgagtgtg	gtagaatatac	aataaatgac	tcgtttcggc	960
ggcggttggt	atgccacatt	atatgtctta	gtgtctatca	gaattcgaat	ttgatttata	1020
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<210> 4

<211> 228

<212> PRT

<213> Calendula officinalis

<400> 4

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Val	Glu	Lys	Gly	Trp	Ser	Pro	Met	Thr	Gly	His	Ser	Ala	Met	Arg	Lys
	20						25						30		

Thr	Leu	Gln	Ser	Leu	Leu	Phe	Arg	Cys	Ser	Lys	Phe	Lys	Ile	Lys	Ala
		35				40						45			

Val	Ser	Ile	Tyr	Ala	Phe	Ser	Thr	Glu	Asn	Trp	Thr	Arg	Pro	Lys	Glu
		50				55					60				

Glu	Val	Asp	Phe	Leu	Met	Glu	Met	Tyr	Glu	Asp	Leu	Leu	Arg	Thr	Asp
	65				70			75					80		

Ala	Glu	Glu	Leu	Leu	Ser	Leu	Gly	Cys	Arg	Val	Ser	Ile	Met	Gly	Lys
		85				90						95			

Lys	Thr	Asn	Leu	Pro	Lys	Ser	Leu	Gln	Lys	Leu	Cys	Ile	Glu	Ile	Glu
			100				105					110			

Glu	Lys	Ser	Arg	Ala	Asn	Ser	Gly	Thr	His	Val	Asn	Tyr	Ala	Leu	Asn
	115						120					125			

Tyr	Ser	Gly	Lys	Tyr	Asp	Ile	Ile	Glu	Ala	Cys	Lys	Ser	Val	Ala	Thr
	130				135						140				

Lys	Val	Lys	Asp	Gly	Val	Ile	Ile	Pro	Lys	Gln	Ile	Asp	Glu	Lys	Tyr
145					150				155			160			

Phe	Lys	Gln	Glu	Leu	Gly	Thr	Lys	Met	Ile	Asp	Phe	Pro	Tyr	Pro	Asp
		165				170			170			175			

Leu	Val	Ile	Arg	Thr	Ser	Gly	Glu	Ile	Arg	Leu	Ser	Asn	Phe	Met	Leu
		180				185						190			

Trp	Gln	Met	Ala	Tyr	Ser	Glu	Leu	Tyr	Phe	Thr	Asp	Lys	Tyr	Phe	Pro
	195					200					205				

Asp	Phe	Gly	Glu	Asn	Asp	Leu	Ile	Glu	Ala	Leu	Leu	Ala	Phe	Gln	Lys
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Val Arg Lys Cys
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<210> 5
<211> 1071

<212> DNA

<213> *Hevea brasiliensis*

<400> 5

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taagtcagtg	atthaaggaa	aatggaatta	tacaacggtg	agaggccaag	tgtgttcaga	180
cttttaggga	agatatacgag	aaaagggtta	tatagcatcc	taaccagggg	tcccatccct	240
actcatattg	ccttcataatt	ggatggaaac	aggaggttg	ctaagaagca	taaactgcca	300
gaaggaggtg	gtcataaggc	tggattttt	gctcttctga	acgtactaac	ttattgctat	360
gagttaggag	tgaaatatgc	gactatctat	gccttagca	tcgataattt	tcgaaggaaa	420
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gaagaaagta	tcatcaatgc	atatgatatt	tgcgtacgtt	ttgtggtaa	cctgaagctt	540
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aatgtgtgc	ttctcattgc	tgtatgctat	acttcaactg	atgagatcgt	gcatgctgtt	660
gaagaatct	ctgaattgaa	ctccaaatgaa	gtttagtaaca	atcaagaattt	ggaggaggca	720
aatgcaactg	gaagcagtagc	tgtgatccaa	actgagaaca	tggagtctga	ttctgtaata	780
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aacttccaaac	gtcattattc	ttacttggag	aaacataagg	aatactaaa	ataatttggt	1020
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<210> 6

<211> 290

<212> PRT

<213> *Hevea brasiliensis*

<400> 6

Met Glu Leu Tyr Asn Gly Glu Arg Pro Ser Val Phe Arg Leu Leu Gly
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Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
20 25 30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
 35 40 45

Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala
50 55 60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
65 70 75 80

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
85 90 95

Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
100 105 110

Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
115 120 125

Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
130 135 140

Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
145 150 155 160

Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
165 170 175

Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
 180 185 190

Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
195 200 205

Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
210 215 220

Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
225 230 235 240

Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
245 250 255

Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
260 265 270

Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
275 280 285

Leu Lys
290

<210> 7

<211> 1000

<212> DNA

<213> Hevea brasiliensis

<400> 7

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tcatggaaga	aagtatcatc	aatgcata	atatttgcgt	acgttttgtg	ggtaacctga	420
agctttaag	tgagccagtc	aagaccgcag	cagataagat	tatgagggtc	actgcaca	480
attccaaatg	tgtgcttctc	attgctgtat	gctatacttc	aactgatgag	atcgtgcatg	540
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<210> 8

<211> 290

<212> PRT

<213> Hevea brasiliensis

<400> 8

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Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
20 25 30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
35 40 45

Lys His Lys Leu Pro Glu Gly Gly His Lys Ala Gly Phe Leu Ala
50 55 60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
65 70 75 80

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
85 90 95

Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
100 105 110

Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
115 120 125

Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
130 135 140

Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
145 150 155 160

Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
165 170 175

Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
180 185 190

Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
195 200 205

Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
210 215 220

Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
225 230 235 240

Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
245 250 255

Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
260 265 270

Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
275 280 285

Leu Lys
290

<210> 9
<211> 1000
<212> DNA
<213> Hevea brasiliensis

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catgagaaaa gggttatata gcatcctaac ccaaggccc atccctactc atcttgccct 180
cataatggat ggaacccgga ggttgctaa gaagcacaaa atgaaagaag cagaaggta 240
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tcgaacttct gggttggcc gtctaaatctt ctacctactt tggcagacta gtaattgcatt 840
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<210> 10
 <211> 296
 <212> PRT
 <213> Hevea brasiliensis

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 20 25 30

Pro Thr His Leu Ala Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Lys 300
 35 40 45

Lys His Lys Met Lys Glu Ala Glu Gly Tyr Lys Ala Gly Tyr Leu Ala 500
 50 55 60

Leu Leu Arg Thr Leu Thr Tyr Cys Tyr Glu Leu Gly Val Arg Tyr Val 600
 65 70 75 80

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Gln Pro Arg Glu 800
 85 90 95

Val Gln Cys Val Met Asn Leu Met Met Glu Lys Ile Glu Glu Ile Ile 1000
 100 105 110

Val Glu Glu Ser Ile Met Asn Ala Tyr Asp Val Gly Val Arg Ile Val 1200
 115 120 125

Gly Asn Leu Asn Leu Asp Glu Pro Ile Arg Ile Ala Ala Glu Lys 1400
 130 135 140

Ile Met Arg Ala Thr Ala Asn Asn Ser Gly Phe Val Leu Leu Ile Ala 1600
 145 150 155 160

Val Ala Tyr Ser Ser Thr Asp Glu Ile Gly His Ala Val Glu Glu Ser 1800
 165 170 175

Ser Lys Asp Lys Leu Asn Ser Asn Glu Val Cys Asn Asn Gly Ile Glu 2000
 180 185 190

Ala Glu Gln Glu Phe Lys Glu Ala Asn Gly Thr Gly Asn Ser Val Ile 2200
 195 200 205

Pro Val Gln Lys Thr Glu Ser Tyr Ser Gly Ile Asn Leu Ala Asp Leu 2400
 210 215 220

Glu Lys Asn Thr Tyr Val Asn Pro His Pro Asp Val Leu Ile Arg Thr 2600
 225 230 235 240

Ser Gly Leu Ser Arg Leu Ser Asn Tyr Leu Leu Trp Gln Thr Ser Asn 2800
 245 250 255

Cys Ile Leu Tyr Ser Pro Phe Ala Leu Trp Pro Glu Ile Gly Leu Arg 3000
 260 265 270

His Leu Val Trp Thr Val Met Asn Phe Gln Arg His His Ser Tyr Leu 3200
 275 280 285

Glu Lys His Lys Glu Tyr Leu Lys
290 295

<210> 11
<211> 1232
<212> DNA
<213> Vitis sp

<400> 11
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aagtaacaga atcgattcat tttctttcc tccaatctca gttcccagat ttcacaaaact 180
tcgcacagct aaaactgatg tagttgggaa agaagaagca agagaagtaa acgagagagc 240
ggaggaattt ccggacggtc ttccggagaga actgatgccc gaacacgtgg ccgtcattat 300
ggacggaaac gtgaggtggg cacagaagag ggggttgcgg gcggcgtcgg gtcaccaagc 360
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ctcggtttc gcattttcct atgataatttgc tgcgttcc gaaggggagg ttggttttct 480
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gaaggatgag tttgtggagg ctttaagttc ttttcagaaaa aggccagagac gatatgggg 960
gcaaaaactga gttactaat tacatataaga tccccaaactt ctgctccatt catatggaga 1020
acttgtatac cattatataa agttaaatttgc ctgagaatttgc acttattaca cacagatccc 1080
caacctatac tccattcata tggaaaactt gtaccattat atgaaactca ttcttcagaa 1140
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<210> 12
<211> 309
<212> PRT
<213> Vitis sp

<400> 12
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1 5 10 15
Met Leu Ser Phe Arg Phe Pro Ile Ser Ala Asp Asn Ala Arg His Thr
1 5 10 15
Phe Lys Ser Lys His Ser Ser Cys Thr Phe Arg Ser Asn Arg Ile Asp
20 25 30
Phe Lys Ser Lys His Ser Ser Cys Thr Phe Arg Ser Asn Arg Ile Asp
20 25 30
Ser Phe Ser Phe Pro Pro Ile Ser Val Pro Arg Phe His Lys Leu Arg
35 40 45
Ser Phe Ser Phe Pro Pro Ile Ser Val Pro Arg Phe His Lys Leu Arg
35 40 45
Thr Ala Lys Thr Asp Val Val Gly Glu Glu Ala Arg Glu Val Asn
50 55 60
Thr Ala Lys Thr Asp Val Val Gly Glu Glu Ala Arg Glu Val Asn
50 55 60
Glu Arg Ala Glu Glu Phe Pro Asp Gly Leu Arg Arg Glu Leu Met Pro
65 70 75 80
Glu Arg Ala Glu Glu Phe Pro Asp Gly Leu Arg Arg Glu Leu Met Pro
65 70 75 80
Glu His Val Ala Val Ile Met Asp Gly Asn Val Arg Trp Ala Gln Lys
85 90 95
Glu His Val Ala Val Ile Met Asp Gly Asn Val Arg Trp Ala Gln Lys
85 90 95
Arg Gly Leu Pro Ala Ala Ser Gly His Gln Ala Gly Val Arg Ser Leu
100 105 110
Arg Gly Leu Pro Ala Ala Ser Gly His Gln Ala Gly Val Arg Ser Leu
100 105 110
Arg Glu Leu Val Glu Leu Cys Cys Lys Trp Gly Ile Lys Val Leu Ser
115 120 125

Val Phe Ala Phe Ser Tyr Asp Asn Trp Ser Arg Ser Glu Gly Glu Val
 130 135 140
 Gly Phe Leu Met Ser Leu Ile Glu Arg Val Val Lys Ala Glu Leu Pro
 145 150 155 160
 Ile Leu Gly Gly Lys Ala Phe Glu Cys Arg Asp Trp Gly Phe Val Lys
 165 170 175
 Ala Ser Glu Gln Leu Gln Leu Ile Ile Asp Val Glu Glu Thr Thr Lys
 180 185 190
 Glu Asn Ser Arg Leu Gln Phe Ile Val Ala Leu Ser Tyr Ser Gly Gln
 195 200 205
 Cys Asp Ile Leu Gln Ala Cys Lys Asn Ile Gly His Lys Val Lys Asp
 210 215 220
 Gly Leu Ile Glu Pro Glu Asp Ile Asn Lys Ser Leu Ile Glu Gln Glu
 225 230 235 240
 Leu Gln Thr Asn Cys Thr Glu Phe Pro Phe Pro Asp Leu Leu Ile Arg
 245 250 255
 Thr Ser Gly Glu Leu Arg Val Ser Asn Phe Met Leu Trp Gln Ile Ala
 260 265 270
 Tyr Thr Glu Leu Cys Phe Phe Ser Thr Leu Trp Pro Asp Phe Gly Lys
 275 280 285
 Asp Glu Phe Val Glu Ala Leu Ser Ser Phe Gln Lys Arg Gln Arg Arg
 290 295 300
 Tyr Gly Gly Arg Asn
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 <212> DNA
 <213> Oryza sativa

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 atgggcgtga agtatatcac ggtgtatgca tttagcatcg ataattttaa gcgagatccg 240
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 agaaatgtca tcaacaaggt taactgtaag atcaacttct ggggaaactt ggacatgtt 360
 agcaaatcag tgagggttagc agctgagaaa ctgatggcta ccactgctga aaacacggga 420
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 aatggtggt attcagacat ttcaagtggca gatctggacc gccatatgtc cagcgcttgt 600
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Ala Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr
35 40 45

Ile Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr
50 55 60

Glu Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu
65 70 75 80

Leu Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe
85 90 95

Trp Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu
100 105 110

Lys Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val
115 120 125

Cys Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys
130 135 140

Val Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser
145 150 155 160

Val Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp
165 170 175

Arg His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg
180 185 190

Thr Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr
195 200 205

Phe Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe
210 215 220

Lys His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser
225 230 235 240

Ile Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
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<212> DNA
<213> Oryza sativa

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gctgtccctc cgtatggccc aatgcctaag catattgcat ttattatgga tggtaaccgt 180

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 gaggaaaaga tcaatgact gctagaaaac agaaatgtca tcaacaaggta 420
 atcaacttct ggggaactt ggacatgttgc agcaaattcag tgagggttagc agctgagaaa 480
 ctgatggcta ccactgctga aaacacggga ctggcttct ctgtttgc 540
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 tcaggtgaga ctgcgcctgag caatttcctt ctgtggcaga cgcacgttc 780
 aatccagacc ctcttggcc ggagttctt ttcaagcacc ttgtctggc cataactccag 840
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 <211> 299
 <212> PRT
 <213> Oryza sativa

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 Asn Phe Ile Arg Lys Cys Ile Val Ala Val Leu Ser Tyr Gly Pro Met
 35 40 45

 Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala Lys
 50 55 60

 Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser Ala
 65 70 75 80

 Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr Ile
 85 90 95

 Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr Glu
 100 105 110

 Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu Leu
 115 120 125

 Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe Trp
 130 135 140

 Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu Lys
 145 150 155 160

 Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val Cys
 165 170 175

 Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys Val
 180 185 190

 Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser Val
 195 200 205

 Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp Arg
 210 215 220

 His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg Thr
 225 230 235 240

Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr Phe
245 250 255

Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe Lys
260 265 270

His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser Ile
275 280 285

Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
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<210> 17

<211> 1028

<212> DNA

<213> Glycine max

<400> 17

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cccaaacaca	gagttttatc	gtctcgaaagc	gcgggtccgc	cattgcgaag	tgtcacgtg	240
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cggcggacta	cgcggcggag	atgatgcca	agcatgtggc	ggtgataatg	gacggaaacg	360
ggaggtggc	gaaggtgaag	gggctgccac	catggcgggg	gcaccaggcg	ggggtgcaat	420
cgctgaggaa	aatggtgagg	ctgtgttgc	gctggggat	taagttctt	acggttttcg	480
cgttctctac	ggataactgg	gttcgcccc	aggtggaggt	tgatttcttgc	atgaggctgt	540
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tgattggaga	ttcatcaagg	ttgcctgagt	ctttaaaaag	aatgatagct	agtgcagaag	660
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tggatgacat	aaacgaaaac	attattgaac	aagaatttgg	aactaattgt	actgagttc	840
cttattcctga	tctactaata	cgaacttagt	gcgagcttag	agtgagtaac	ttcttgttgc	900
ggcaatttagc	ctacacagaa	ctttatTTA	atcgggaact	ctggccagat	tttgggaagg	960
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<211> 322

<212> PRT

<213> Glycine max

<400> 18

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Cys Tyr His Pro Phe His His Arg Ser Gln Thr Gln Ser Leu Ile Val						
35	40	45				

Ser Lys Arg Gly Ser Ala Ile Ala Lys Cys His Ala Asp Ser Val Thr						
50	55	60				

Leu Arg Asp Asp Gly Val Ser Leu Ala Gln Glu Ser Leu Glu Pro Leu						
65	70	75	80			

Pro Ala Glu Leu Ala Ala Glu Met Met Pro Lys His Val Ala Val Ile						
85	90	95				

Met Asp Gly Asn Gly Arg Trp Ala Lys Val Lys Gly Leu Pro Pro Ser
 100 105 110
 Ala Gly His Gln Ala Gly Val Gln Ser Leu Arg Lys Met Val Arg Leu
 115 120 125
 Cys Cys Ser Trp Gly Ile Lys Val Leu Thr Val Phe Ala Phe Ser Thr
 130 135 140
 Asp Asn Trp Val Arg Pro Lys Val Glu Val Asp Phe Leu Met Arg Leu
 145 150 155 160
 Phe Glu Arg Thr Ile Asn Ser Glu Val Gln Thr Phe Lys Arg Glu Gly
 165 170 175
 Ile Arg Ile Ser Val Ile Gly Asp Ser Ser Arg Leu Pro Glu Ser Leu
 180 185 190
 Lys Arg Met Ile Ala Ser Ala Glu Glu Asp Thr Lys Gln Asn Ser Arg
 195 200 205
 Phe Gln Leu Ile Val Ala Val Gly Tyr Ser Gly Lys Tyr Asp Val Val
 210 215 220
 Gln Ala Cys Lys Ser Val Ala Lys Lys Val Lys Asp Gly His Ile His
 225 230 235 240
 Leu Asp Asp Ile Asn Glu Asn Ile Ile Glu Gln Glu Leu Glu Thr Asn
 245 250 255
 Cys Thr Glu Phe Pro Tyr Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
 260 265 270
 Leu Arg Val Ser Asn Phe Leu Leu Trp Gln Leu Ala Tyr Thr Glu Leu
 275 280 285
 Tyr Phe Asn Arg Glu Leu Trp Pro Asp Phe Gly Lys Asp Glu Phe Val
 290 295 300
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 His Ser
 <210> 19
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 <212> DNA
 <213> Triticum aestivum
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 aaaaaaa 1026

<210> 20
 <211> 266
 <212> PRT
 <213> *Triticum aestivum*

<400> 20
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 20 25 30

Arg His Val Ala Leu Val Met Asp Gly Asn Ser Arg Trp Ala Ala Ala
 35 40 45

Arg Gly Leu Pro Pro Thr Asp Gly His Glu His Gly Met Arg Ala Leu
 50 55 60

Met Arg Thr Val Arg Leu Ser Arg Ala Trp Gly Ile Arg Val Leu Thr
 65 70 75 80

Ala Phe Gly Phe Ser Leu Glu Asn Trp Asn Arg Pro Lys Ala Glu Val
 85 90 95

Asp Phe Leu Met Ala Leu Ile Glu Arg Phe Ile Asn Asp Asn Leu Ala
 100 105 110

Glu Phe Leu Arg Glu Gly Thr Arg Leu Arg Ile Ile Gly Asp Arg Ser
 115 120 125

Arg Leu Pro Ile Ser Val Gln Lys Thr Ala Arg Asp Ala Glu Glu Ala
 130 135 140

Thr Arg Asn Asn Ser Gln Leu Asp Leu Val Leu Ala Ile Ser Tyr Ser
 145 150 155 160

Gly Arg Met Asp Ile Val Gln Ala Cys Arg Asn Leu Ala Gln Lys Val
 165 170 175

Asp Ala Lys Leu Leu Arg Pro Glu Asp Ile Asp Glu Ser Leu Phe Ala
 180 185 190

Asp Glu Leu Gln Thr Ser Glu Thr Ser Cys Pro Asp Leu Leu Ile Arg
 195 200 205

Thr Ser Gly Glu Leu Arg Leu Ser Asn Phe Leu Leu Trp Gln Ser Ala
 210 215 220

Tyr Ser Glu Leu Phe Phe Thr Asp Thr Leu Trp Pro Asp Phe Gly Glu
 225 230 235 240

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<300>
<301> Apfel, C. M.
<302> Use of Genomics to Identify Bacterial Undecaprenyl Pyrophosphate Synthetase: Cloning, Expression, and Characterization of the Essential uppS Gene
<303> J. Bacteriol.
<304> 81
<306> 483-492
<307> 1999

<400> 21
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<210> 22
<211> 24
<212> PRT
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<220>
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Leu Trp Gln Xaa Xaa Tyr Xaa Glu
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<210> 23
<211> 750
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<213> *Micrococcus luteus*

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<301> Shimizu, N.
<302> Molecular Cloning, Expression, and Purification of Undecprenyl
Diphosphate Synthase: No Sequence Similarity between E- and
Z-prenyl Diphosphate Synthases
<303> J. Biol. Chem.
<304> 273
<306> 19476-19481
<307> 1998

<400> 23
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<212> PRT
<213> *Micrococcus luteus*

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Arg Trp Ala Lys Gln Lys Lys Met Pro Arg Ile Lys Gly His Tyr Glu
35 40 45
Gly Met Gln Thr Val Lys Lys Ile Thr Arg Tyr Ala Ser Asp Leu Gly
50 55 60
Val Lys Tyr Leu Thr Leu Tyr Ala Phe Ser Thr Glu Asn Trp Ser Arg
65 70 75 80

Pro Lys Asp Glu Val Asn Tyr Leu Met Lys Leu Pro Gly Asp Phe Leu
 85 90 95
 Asn Thr Phe Leu Pro Glu Leu Ile Glu Lys Asn Val Lys Val Glu Thr
 100 105 110
 Ile Gly Phe Ile Asp Asp Leu Pro Asp His Thr Lys Lys Ala Val Leu
 115 120 125
 Glu Ala Lys Glu Lys Thr Lys His Asn Thr Gly Leu Thr Leu Val Phe
 130 135 140
 Ala Leu Asn Tyr Gly Gly Arg Lys Glu Ile Ile Ser Ala Val Gln Leu
 145 150 155 160
 Ile Ala Glu Arg Tyr Lys Ser Gly Glu Ile Ser Leu Asp Glu Ile Ser
 165 170 175
 Glu Thr His Phe Asn Glu Tyr Leu Phe Thr Ala Asn Met Pro Asp Pro
 180 185 190
 Glu Leu Leu Ile Arg Thr Ser Gly Glu Glu Arg Leu Ser Asn Phe Leu
 195 200 205
 Ile Trp Gln Cys Ser Tyr Ser Glu Phe Val Phe Ile Asp Glu Phe Trp
 210 215 220
 Pro Asp Phe Asn Glu Glu Ser Leu Ala Gln Cys Ile Ser Ile Tyr Gln
 225 230 235 240
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 <213> *Saccharomyces cerevisiae*

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 20 25 30
 Arg His Val Gly Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Arg Lys
 35 40 45
 Lys Glu Met Asp Val Lys Glu Gly His Glu Ala Gly Phe Val Ser Met
 50 55 60
 Ser Arg Ile Leu Glu Leu Cys Tyr Glu Ala Gly Val Asp Thr Ala Thr
 65 70 75 80
 Val Phe Ala Phe Ser Ile Glu Asn Phe Lys Arg Ser Ser Arg Glu Val
 85 90 95
 Glu Ser Leu Met Thr Leu Ala Arg Glu Arg Ile Arg Gln Ile Thr Glu
 100 105 110
 Arg Gly Glu Leu Ala Cys Lys Tyr Gly Val Arg Ile Lys Ile Ile Gly
 115 120 125
 Asp Leu Ser Leu Leu Asp Lys Ser Leu Leu Glu Asp Val Arg Val Ala
 130 135 140
 Val Glu Thr Thr Lys Asn Asn Lys Arg Ala Thr Leu Asn Ile Cys Phe
 145 150 155 160
 Pro Tyr Thr Gly Arg Glu Glu Ile Leu His Ala Met Lys Glu Thr Ile
 165 170 175
 Val Gln His Lys Lys Gly Ala Ala Ile Asp Glu Ser Thr Leu Glu Ser
 180 185 190
 His Leu Tyr Thr Ala Gly Val Pro Pro Leu Asp Leu Leu Ile Arg Thr
 195 200 205
 Ser Gly Val Ser Arg Leu Ser Asp Phe Leu Ile Trp Gln Ala Ser Ser
 210 215 220
 Lys Gly Val Arg Ile Glu Leu Leu Asp Cys Leu Trp Pro Glu Phe Gly
 225 230 235 240
 Pro Ile Arg Met Ala Trp Ile Leu Leu Lys Phe Ser Phe His Lys Ser
 245 250 255
 Phe Leu Asn Lys Glu Tyr Arg Leu Glu Glu Gly Asp Tyr Asp Glu Glu
 260 265 270
 Thr Asn Gly Asp Pro Ile Asp Leu Lys Glu Lys Lys Leu Asn
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<400> 27

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ttaagggtag	ggccagtgcc	tgaacatgtc	tcctttatca	tggatggtaa	ccggagatat	240
gccaagtcaa	gaaggctacc	agtaaaaaaa	ggccatgaag	ctgggtgggtt	aacgttacta	300
acactactgt	atatctgcaa	aagattgggt	gtaaaatgtg	tttcgccta	tgcattttct	360
attgaaaatt	ttaatagacc	aaaagaagaa	gtagatacgc	taatgaattt	gtttacggta	420
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<211> 343

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 28

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					20				25					30	

Phe	Gln	Arg	Val	Phe	Ala	Trp	Val	Met	Ser	Leu	Ser	Leu	Phe	Ser	Trp
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Phe	Tyr	Val	Asn	Leu	Gln	Asn	Ile	Leu	Ile	Lys	Ala	Leu	Arg	Val	Gly
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Pro	Val	Pro	Glu	His	Val	Ser	Phe	Ile	Met	Asp	Gly	Asn	Arg	Arg	Tyr
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Ala	Lys	Ser	Arg	Arg	Leu	Pro	Val	Lys	Lys	Gly	His	Glu	Ala	Gly	Gly
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Leu	Thr	Leu	Leu	Thr	Leu	Leu	Tyr	Ile	Cys	Lys	Arg	Leu	Gly	Val	Lys
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Cys	Val	Ser	Ala	Tyr	Ala	Phe	Ser	Ile	Glu	Asn	Phe	Asn	Arg	Pro	Lys
							115		120					125	

Glu	Glu	Val	Asp	Thr	Leu	Met	Asn	Leu	Phe	Thr	Val	Lys	Leu	Asp	Glu
						130			135					140	

Phe	Ala	Lys	Arg	Ala	Lys	Asp	Tyr	Lys	Asp	Pro	Leu	Tyr	Gly	Ser	Lys
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Ile	Arg	Ile	Val	Gly	Asp	Gln	Ser	Leu	Leu	Ser	Pro	Glu	Met	Arg	Lys
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Lys	Ile	Lys	Lys	Val	Glu	Glu	Ile	Thr	Gln	Asp	Gly	Asp	Asp	Phe	Thr
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Leu	Phe	Ile	Cys	Phe	Pro	Tyr	Thr	Ser	Arg	Asn	Asp	Met	Leu	His	Thr
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Ile Arg Asp Ser Val Glu Asp His Leu Glu Asn Lys Ser Pro Arg Ile
210 215 220

Asn Ile Arg Lys Phe Thr Asn Lys Met Tyr Met Gly Phe His Ser Asn
225 230 235 240

Lys Cys Glu Leu Leu Ile Arg Thr Ser Gly His Arg Arg Leu Ser Asp
245 250 255

Tyr Met Leu Trp Gln Val His Glu Asn Ala Thr Ile Glu Phe Ser Asp
260 265 270

Thr Leu Trp Pro Asn Phe Ser Phe Ala Met Tyr Leu Met Ile Leu
275 280 285

Lys Trp Ser Phe Phe Ser Thr Ile Gln Lys Tyr Asn Glu Lys Asn His
290 295 300

Ser Leu Phe Glu Lys Ile His Glu Ser Val Pro Ser Ile Phe Lys Lys
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<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 29

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32

<210> 30

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<212> DNA

<213> Artificial Sequence

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<210> 31

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<212> DNA

<213> Artificial Sequence

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26

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<213> arabidopsis

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